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December 26, 2001, 10:35:29 ; Search time 9.67 Seconds (without alignments) 611.308 Million cell updates/sec
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Sequence 54, Appl
Sequence 61, Appli
Sequence 57, Appl
Sequence 58, Appl
Sequence 58, Appl
Sequence 60, Appl
Sequence 60, Appl
Sequence 17, Appl
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Sequence 17, Appl
Sequence 17, Appl
Sequence 6, Appli
Sequence 18, Appli
Sequence 16, Appli
Sequence 16, Appli
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1: /cgn2_6/ptodata/2/paa/PCT_NEW_COMB.pep:*

3: /cgn2_6/ptodata/2/paa/USO6_NEW_COMB.pep:*

3: /cgn2_6/ptodata/2/paa/USO8_NEW_COMB.pep:*

3: /cgn2_6/ptodata/2/paa/USO8_NEW_COMB.pep:*

5: /cgn2_6/ptodata/2/paa/USO8_NEW_COMB.pep:*

5: /cgn2_6/ptodata/2/paa/USO8_NEW_COMB.pep:*

7: /cgn2_6/ptodata/2/paa/USO8_NEW_COMB.pep:*

7: /cgn2_6/ptodata/2/paa/USO8_NEW_COMB.pep:*
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd
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US-09-497-967-54

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US-09-497-967-60

US-09-497-967-60

US-09-497-967-60

US-09-975-113-47

US-09-975-12

US-09-975-12

US-09-977-053-4

US-09-977-053-6

US-09-977-967-10

US-09-976-594-616

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US-09-976-594-616

US-09-976-594-616
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Maximum Match 100%
Listing first 45 summaries

    protein search, using sw model

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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Clark, Theodore G.
APPLICANT: Dickerson, Jr., Harry W.
APPLICANT: Lin, Tian-Long
ITTLE OF INVENTION: DIAGNOSTIC AND PROTECTIVE ANTIGEN GENE SEQUENCES OF
TITLE OF INVENTION: LICHTHVOPHTHIRUS
FILE REFERENCE: 235.00170101
CURRENT APPLICATION NUMBER: 05/09/497,967
FILE REFERENCE: 1999-00-02-04
PRIOR PLICATION NUMBER: 60/131,121
PRIOR PAPLICATION NUMBER: 60/118,634
PRIOR FILING DATE: 1999-02-04
PRIOR PELING DATE: 1999-02-04
PRIOR PELING DATE: 1999-03-02
PRIOR PELING DATE: 1999-03-02
PRIOR PELING DATE: 1999-03-02
SPROR PELING DATE: 1999-03-07
SPROR PELING DATE: 1999-03-07
SPROR PELING DATE: 1999-03-07
SPROR FILING DATE: 1999-03-17
SPROR FILING DATE: 1999-03-17 ö 12, Appl 14, Appl 16, Appl 16, Appl 106, Appl 106, App 22, Appl 21, Appl 119, Appl 21, Appl 31, Appl 3 Gaps 1 MKNNILVILIISLFINQIKSANCPVGTETNTAGQVDDLGTPANCVNCQKNFYYNNAAAFV 60 sednence sed ö Length 468 Indels Query Match 100.0%; Score 2540; DB 5; Best Local Similarity 100.0%; Pred. No. 7.9e-199; Matches 468; Conservative 0; Mismatches 0; US-09-500-746-19
US-09-898-570-11
US-09-898-570-10
US-09-898-570-14
US-09-898-570-14
US-09-898-570-14
US-09-898-570-14
US-09-898-570-14
US-09-898-570-16
US-09-991-496-52
US-09-991-498-6-488-21
US-09-800-4498-6
US-09-900-4498-6
US-09-900-4498-6 ALIGNMENTS ; TYPE: PRT ; ORGANISM: Ichthyophthirius multifiliis US-09-497-967-7 845 974 1009 83 392 1169 320 320 610 871 871 871 556 639 V 0 4 4 4 4 0 0 0 0 0 V V V V 0 0 0 V V 4 468 RESULT 1 US-09-497-967-7 170 162.5 162.5 162.5 162.5 162.5 153 153 153 153 153 144 144.5 144.5 144.5 144.5 144.5 142.5 142.5 142.5 143.5 143.5 q ò qq

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Matches 214;
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GENERAL INFORMATION:
APPLICANT: Clark, Theodore G.
APPLICANT: Dickerson, Jr., Harry W.
APPLICANT: Dickerson, Jr., Harry W.
APPLICANT: Dickerson, Jr., Harry W.
APPLICANT: Lin, Than-Long
TITLE OF INVENTION: DIAGNOSTIC AND PROTECTIVE ANTIGEN GENE SEQUENCES OF
TITLE OF INVENTION: ICHTHYOPHTHIRUS
FILE REFERENCE: 235.0017010.
CURRENT APPLICATION NUMBER: US/09/497,967
CURRENT FILING DATE: 2000-02-04
PRIOR PILING DATE: 1999-04-27
PRIOR APPLICATION NUMBER: 60/112,372
PRIOR APPLICATION NUMBER: 60/122,372
PRIOR PLILNG DATE: 1999-03-07
PRIOR PLILNG DATE: 1999-03-07
PRIOR PLILNG DATE: 1999-03-07
PRIOR PLILNG DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 102
SOFTWARE: Patentin Ver: 2.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NEYNENAPNENAGASTCTACPVNRVGGALTAGNAATIVAQCNVACPTGTALDDGVTTDYV 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MKNNILVILLISLFINQIKSANCPVGTETNTAGQVDDLGTPANCVNCQKNFYYNNAAAFV 60
                                                                                360
                                                                                                           361 VQGAVATAGGTATLIAQCALECPAGTVLTDGTTSTYKQAASECVKCAANFYTTKQTDWVA 420
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                  AATLAKQCNIACPDGTAIASGATNYVILQTECLNCAANFYFDGNNFQAGSSRCKACPANK
                                                                       CPDGTISAAGVNNWVAQNTECTNCAPNFYNNNAPNFNPGNSTCLPCPANKDYGAEATAGG
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                                                                                                                                                               OTHER INFORMATION: Description of Artificial Sequence: , OTHER INFORMATION: proline mutant antigen protein US-09-497-967-54
                                                                                                                                                                                                                                                         Sequence 54, Application US/09497967
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Artificial Sequence
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Matches 467; Conservative
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APPLICANT CLARK, Theodore G.
APPLICANT DICKETSON, Jr., Harry W.
APPLICANT Lin, Tian-Loop
APPLICANT Lin, Tian-Loop
TITLE OF INVENTION: ICHTHYOPHTHIRIUS
TITLE OF INVENTION: ICHTHYOPHTHIRIUS
FILLE REFERENCE: 235.001/0101
CURRENT APPLICATION NUMBER: 60/204
PRIOR APPLICATION NUMBER: 60/118,634
PRIOR APPLICATION NUMBER: 60/118,634
PRIOR FILING DATE: 1999-04-27
PRIOR FILING DATE: 1999-03-02-04
PRIOR FILING DATE: 1999-03-07
PRIOR FILING DATE: 1999-03-07
PRIOR FILING DATE: 1999-03-07
PRIOR FILING DATE: 1999-03-07
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   222 VAQATLGNDATITAQCNVACPDGTISAAGVNNWVAQNTE---CTNCAPNFYNN-----N 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               117 NCRINFYNENAPNFNAGASTCTACPVNRVGGALTAGNAATIVAQCNVACPTGTALDDGVT 176
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               57 AAFVPGASTCTPCPQKKDAGAQPNPPATANLVTQCNVKCPAGTAIAGGATDYAAIITECV 116
                                                                                                                         1 MKNNILVILIISLFINQIKSANCPVGTETNTAGQVD----DLGTPANCVNCQKNFYYNNA 56
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                                                                                               361 VQGAVATAGGTATLIAQCALECPAGTVLTDGTTSTYKQAASECVKCAANFYTTKQTDWVA
                               45; Mismatches 139; Indels 114;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 442;
                                                                                                                                                                                                                              421 GIDTCTSCNKKLTSGAEANLPESAKKNIQCDFANFLSISLLLISYYLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            36.3%; Score 921; DB 5; 41.8%; Pred. No. 1.1e-67;
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                                                                                                                                                                                                                                                                                                                                                          US-09-497-967-6; Sequence 6, Application US/09497967; GENERAL INFORMATION:
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354 ECTKCSAGFFASKTTGFTAGTDTCTECTKKLTSGATAKVYAEATQKVQCASTTF 407
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                                                                                                      Sequence 57, Application US/09497967
GENERAL INFORMATION:
APPLICANT: Clark, Theodore G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             225 ATLGNDATITAQCNVA 240
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Matches 76; Conserv
                                                               RESULT 5
US-09-497-967-57
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US-09-497-967-55
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APPLICANT: CLARK Theodore G.
APPLICANT: Dickerson, Jr., Harry W.
APPLICANT: Dickerson, Jr., Harry W.
APPLICANT: Lin, Tian-Long
TITLE OF INVENTION: DIGNOSTIC AND PROTECTIVE ANTIGEN GENE SEQUENCES OF
TITLE OF INVENTION: ICHTWOPHTHINUS
FILE REFERENCE: 235.00170101
CURRENT APPLICATION NUMBER: 0S/09/497,967
CURRENT APPLICATION NUMBER: 60/131,121
PRIOR APPLICATION NUMBER: 60/131,121
PRIOR APPLICATION NUMBER: 60/123,372
PRIOR FILING DATE: 1999-02-04
PRIOR PELING DATE: 1999-03-02
PRIOR PLING DATE: 1999-03-02
PRIOR FILING DATE: 1999-03-02
SPROR FILING DATE: 1999-03-02
SOFTWARE: PALENTIN NUMBER: 60/124,905
SOFTWARE: PALENTIN VOICE: 102
SOFTWARE: PALENTIN VOICE: 102
SOFTWARE: PALENTIN VOICE: 103
SOFTWARE: PALENTIN VOICE: 103
SOFTWARE: PALENTIN VOICE: 103
SOFTWARE: PALENTIN VOICE: 2.1
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                                380 LECPAGTVLTDGTTSTYKQAASECVKCAANFYTTKQTDWVAGIDTCTSCNKKLTSGAEAN 439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        79 PNPPATANLVTQCNVKCPAGTAIAGGATDYAAIITECVNCRINFYNENAPNFNAGASTCT 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        139 ACPVNRVGGALTAGNAATIVAQCNVACPTGTALDDGVTTDYVRSFTECVKCRLNFYYNGN 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   199 N--GNTP----FNPG------KSQCTPCPAIKPANVAQATLGNDATITAQCNVACPD 243
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31.6%; Score 801.5; DB 5; Length 409;
Best Local Similarity 39.5%; Pred. No. 4.8e-58;
Matches 187; Conservative 39; Mismatches 137; Indels 111;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ECVKCAANFYTTKQTDWVAGIDTCTSCNKKLTSGAEANLPESAKKNIQCDFANF 455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   45 GNOPFAAN------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Ichthyophthirius multifillis US-09-497-967-61
                                                                                                                                                                                                           US-09-497-967-61; Sequence 61, Application US/09497967; GENERAL INFORMATION:
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APPLICANT: Dickerson, Jr. Headly W.
APPLICANT: Lin, Tian-Long
TITLE OF INVENTION: DIAGNOSTIC AND PROTECTIVE ANTIGEN GENE SEQUENCES OF
TITLE OF INVENTION: DIAGNOSTIC AND PROTECTIVE ANTIGEN GENE SEQUENCES OF
TITLE OF INVENTION: DIAGNOSTIC AND PROTECTIVE ANTIGEN GENE SEQUENCES
TITLE OF INVENTION: LITTLY OPPLICATION NUMBER: US/09/497,967
CURRENT APPLICATION NUMBER: 60/131,121
PRIOR PLICATION NUMBER: 60/131,121
PRIOR PLILING DATE: 1999-04-27
PRIOR APPLICATION NUMBER: 60/132,372
PRIOR PLILING DATE: 1999-02-04
PRIOR PLILING DATE: 1999-03-02
PRIOR PLILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 102
SOFTWARE: PATENTIN VET: 2.1
SEQ ID NO 57
LENGTH: 76
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General INFORMATION:
APPLICANT: Clark, Theodore G.
APPLICANT: Lin, Theodore G.
APPLICANT: Lin, Than-Long
TITLE OF INVENTION: ICHTHYOPHTHIRUS
TITLE OF INVENTION: ICHTHYOPHTHIRUS
TITLE OF INVENTION: ICHTHYOPHTHIRUS
TITLE OF INVENTION: ICHTHYOPHTHIRUS
CURRENT APPLICATION NUMBER: US/09/497,967
CURRENT FILING DATE: 1999-04-27
PRIOR PELICATION NUMBER: 60/113,121
PRIOR APPLICATION NUMBER: 60/118,634
PRIOR PILING DATE: 1999-03-02
PRIOR PILING DATE: 1999-03-02
PRIOR PILING DATE: 1999-03-02
PRIOR PILING DATE: 1999-03-03
PRIOR FILING DATE: 1999-03-17
NUMBER: OF SEQ ID NOS: 102
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 55
LENGTH: 72
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ilarity 100.0%; Pred. No. 3.1e-28;
Conservative 0; Mismatches 0;
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US-09-497-967-57
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US-09-497-967-56
                                                                                                                        TYPE: PRT
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| Sequence 60, Application US/09497967
| GENERAL INFORMATION:
| APPLICANT: Clark, Theodore G.
| APPLICANT: Dickerson, Jr., Harry W.
| APPLICANT: Lin, Tian-Long
| TITLE OF INVENTION: ICHTHYOPHTHIRUS
| TITLE OF INVENTION: ICHTHYOPHTHIRUS
| FILE REPERENCE: 235.00170101
| CURRENT FILING DATE: 2000-02-04
| PRIOR APPLICATION NUMBER: 60/131,121
| PRIOR APPLICATION NUMBER: 60/118,634
| PRIOR APPLICATION NUMBER: 60/118,634
| PRIOR APPLICATION NUMBER: 60/123,372
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GENERAL INCOMMENTION:
GENERAL INCOMMENTION:
APPLICANT: Clark, Theodore G.
APPLICANT: Dickerson, Jr., Harry W.
APPLICANT:
TITLE OF INVENTION: DIAGNOSTIC AND PROTECTIVE ANTIGEN GENE SEQUENCES OF
TITLE OF INVENTION: LICHTHYOPHTHIRUS
FILE REFERENCE: 235,00170101
CURRENT APPLICATION NUMBER: 05/131,121
PRIOR APPLICATION NUMBER: 06/131,121
PRIOR PLILING DATE: 1999-04-27
PRIOR FILING DATE: 1999-04-27
PRIOR FILING DATE: 1999-03-04
PRIOR FILING DATE: 1999-03-04
PRIOR FILING DATE: 1999-03-03
PRIOR FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 102
SOFTHARE: PATENTIN VAMPER: 60/124,905
PRIOR FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 102
SOFTHARE: PATENTIN VAMPER: 61/124,905
PRIOR FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 102
SOFTHARE: PATENTIN VAMPER: 61/124,905
PRIOR FILING DATE: 1999-03-17
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                                            Gaps
                                                                                  23 CPVGTETNTAGQVDDLGTPANCVNCQKNFYYNNAAAFVPGASTCTPCPQKKDAGAQPNPP 82
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Query Match
Best Local Similarity 100.0%; Pred. No. 1.2e-26;
Matches 72; Conservative 0; Mismatches 0; Indels
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100.0%; Pred. No. 1.4e-26;
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US-09-497-967-58
                                                                                                                                                                                                                                                                                          RESULT 7
US-09-497-967-58
Sequence 58, Application US/09497967
; SEQUERAL INFORMATION:
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Best Local Similarity 100.0
Matches 71; Conservative
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US-09-497-967-60
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APPLICANT: DIACKSTON, JIT., Harry W.
APPLICANT: DIACKSTON, JT., Harry W.
APPLICANT: Lin, Tian-Long
TITLE OF INVENTION: DIAGNOSTIC AND PROTECTIVE ANTIGEN GENE SEQUENCES OF
TITLE OF INVENTION: ICHTHYOPHTHIRIUS
FILE REPRENCE: 235.00170101
CURRENT PAPLICATION NUMBER: 05/130, 121
PRIOR PAPLICATION NUMBER: 60/131, 121
PRIOR APPLICATION NUMBER: 60/130, 34
PRIOR FILING DATE: 1999-04-27
PRIOR FILING DATE: 1999-02-04
PRIOR FILING DATE: 1999-03-02
PRIOR FILING DATE: 1999-03-02
PRIOR FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 102
SOFTWARE: PATENTIN UNBER: 60/124, 905
PRIOR FILING DATE: 1999-03-17
SOFTWARE: PATENTIN UNBER: 60/124, 905
PRIOR FILING DATE: 1999-03-17
SOFTWARE: PATENTIN UNBER: 60/124, 905
PRIOR FILING DATE: 1999-03-17
SOFTWARE: PATENTIN UNBER: 60/124, 905
PRIOR FILING DATE: 1999-03-17
SOFTWARE: PATENTIN UNBER: 60/124, 905
PRIOR FILING DATE: 1999-03-17
SOFTWARE: PATENTIN UNBER: 60/124, 905
PRIOR FILING DATE: 1999-03-17
SOFTWARE: PATENTIN UNBER: 60/124, 905
PRIOR FILING DATE: 1999-03-17
SOFTWARE: PATENTIN UNBER: 60/124, 905
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                                                                                                                                                                                                                                                                                                                                   Length 72;
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14.8%; Score 375; DB 5; 1
Best Local Similarity 100.0%; Pred. No. 2.6e-24;
Matches 70; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                        15.3%; Score 389; DB 5;
100.0%; Pred. No. 2e-25;
tive 0; Mismatches 0
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                                                                                                                                                                                                                            ORGANISM: Ichthyophthirius multifillis
US-09-497-967-60
PRIOR FILING DATE: 1999-03-02
PRIOR APPLICATION NUMBER: 60/124,905
PRIOR FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 102
SOFTWARE: PATENTIN VEr. 2.1
SEQ ID NO 60
: LENGTH: 72
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Sequence 59, Application US/09497967
GENERAL INFORMATION:
APPLICANT: Clark, Theodore G.
APPLICANT: Dickerson, Jr., Harry W.
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GENERAL INFORMATION:
APPLICANT: Clark, Theodore G.
                                                                                                                                                                                                                                                                                                                                                 Query Match 15.3'
Best Local Similarity 100.
Matches 72; Conservative
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; TYPE: PRT
; ORGANISM: Homo Sapien
PCT-US01-32140-33
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PCT-US01-32140-33
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APPLICANT: Lin, Tian-Long
TITLE OF INVENTION: DIAGNOSTIC AND PROTECTIVE ANTIGEN GENE SEQUENCES OF
TITLE OF INVENTION: IGHTHYOPHTHIRIUS
FILE REFERENCE: 235.001701010
CURRENT ELING DATE: 2000-02-04
CURRENT FILING DATE: 2000-02-04
PRIOR FILING DATE: 1999-04-07
PRIOR FILING DATE: 1999-04-07
PRIOR FILING DATE: 1999-02-04
PRIOR FILING DATE: 1999-03-02
PRIOR FILING DATE: 1999-03-02
PRIOR FILING DATE: 1999-03-07
PRIOR FILING DATE: 1999-03-07
PRIOR FILING DATE: 1999-03-07
PRIOR FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 102
SEQ ID NO 59
LENGTH: 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                312 CPDGTAIASGAINYVILQTECLNCAANFYFDGNNFQAGSSRCKACPANKVQGAVATAGGT 371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       77 AQPNPFATANLVTQCNVKCPAGTAIAGGATDYAAIITECVNCRINFYNENAPNFNAGAST 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            500 CACGCTICAA----TGAGAACAAC-----AGGAGAGTCATTGTTTGCAATACAA 544
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: HSU, Daniel, K.
APPLICANT: HSU, Eu-Tong
APPLICANT: LIU, Fu-Tong
APPLICANT: LIU, Fu-Tong
APPLICANT: LIU, Fu-Tong
APPLICANT: DOWLING, Christopher, A.
TITLE OF INVENTION: GLECTIN EXPRESSION IS INDUCED IN
TITLE OF INVENTION: CIRRHOTIC LIVER AND HEPATOCELLULAR CARCINOMA
FILE REFERENCE: DANHSU: 00AC1
CURRENT FILING DATE: 2001-10-10
PRIOR APPLICATION NUMBER: US/09/975,143
PRIOR FILING DATE: 2000-03-29
NUMBER OF SEQ ID NOS: 47
SOFTHARE: FastESQ for Windows Version 4.0
SEQ ID NO 47
LENGTH: 914
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9.4%; Score 237.5; DB 5; Length 914;
Best Local Similarity 25.7%; Pred. No. 5.6e-12;
Matches 123; Conservative 9; Mismatches 208; Indels 139
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100.0%; Pred. No. 3.8e-24;
1ve 0; Mismatches 0;
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US-09-975-143-47
; Sequence 47, Application US/09975143
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                          Ouery Match
Best Local Similarity 100.
Matches 70; Conservative
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US-09-975-143-47
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586 ITCCCATTTGAAAGTGGGAAACCATTCAAAATACAAGTACTGGTTGAACCTGACCA---- 641
                                                                                                                                                                                                                              680 ACAATCATCGGGTTAAAAACT-CAA-----TGAAATCAGCAAACTGGGAATTTC 728
                                                                                                                                                                                                                                                                                                                                            729 IGGIGACATAGACCICACCAGIGCITCATATACCATGATAAATCIGAAA-----GGGGC 783
                                                                                                                                                                                                                                                                                                                                                                                                      AGSSRCKACPANKVQGAVATAGGTATLIAQCALECPAG-----TVLTDGT---- 392
                                                                                                                                                                                                                                                                                        ---AGGAATLAKQCNIACPDG-----TAIASGATNYVILQTECLNCAANFYFDGNNFQ 347
                                                                                                                                                                                                                                                                                                                                                                                                                                                             784 AGATTAAAAAAAAAAAAAAAAGAATCTAAACCTTACATGTGTAAAGGTTTCATGTTCACTG 843
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3523 GTCGCAACSEQDCAG-----AGACAATGC---CAAGAAACAGCCTCTAC----CTGC--- 3566
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    393 -----TSTYKQAASECVKCA--ANFYTTKQTDWVAG-IDTCTSCNKKLTSGAEA 438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     62 GASTCTPCPQKKDAGAQPNPPATANLVTQCNVKCPAGTAIAGGATDYAAIITECVNCRIN 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 179 YVRSFTECVKCRLNF-----YYNGNNGNTPFNPGKSQCTPCPAIKPANVAQA 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   269 -YNNNAPNFNPGNST-----CLPCPANK------DYGAEATAGGA----ATLAK 306
                                                      192 NEYYNGNNGNTPENPGKSQCTPCPAIKPANVAQATLGNDATITAQCNVACPDGTISAAGV
                                                                                                             3567 -----AGATGAGCAGCCTGAGGGCTGAGGACACCCATGDCATGTATTGGTTT-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEPLICANT: BIOCEN, INC.
APPLICANT: BIOGEN, INC.
APPLICANT: BIOCEN, INC.
APPLICANT: GARBER, Ellen
APPLICANT: LYRE, Paul
APPLICANT: SALDHANA, JOSE W.
TITLE OF INVENTION: HUMANIZED ANTI-LT-BETA-R ANTIBODIES
FILE REFERENCE: A100 PCT
CURRENT APPLICATION NUMBER: PCT/US01/32140
CURRENT FILING DATE: 2001-10-12
PRIOR FILING DATE: 2000-10-13
PRIOR FILING DATE: 2001-00-13
PRIOR FILING DATE: 2001-00-13
PRIOR FILING DATE: 2001-00-13
PRIOR FILING DATE: 2001-06-21
SPRIOR FILING DATE: 2001-06-21
SPRIOR FILING DATE: 2001-06-21
SPRIOR FILING DATE: SOUTHON NUMBER: BALESEQ FOR WINDOWS VERSION 4.0
SEQ ID NO 33
FENENTIAL AREAS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8.8%; Score 222.5; DB 1;
24.8%; Pred. No. 5.4e-10;
tive 11; Mismatches 208;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; Sequence 33, Application PC/TUS0132140 ; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 24.88
Matches 112; Conservative
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Homo sapiens

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US-09-886-055-431
ORGANISM:
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                                                                                                                                                                                                                                                                                                                                                                       GAPLICANT: Clark, Theodore G.
APPLICANT: Clark, Theodore G.
APPLICANT: Clark, Theodore G.
APPLICANT: Lin, Tian-Long Tian-Long
TITLE OF INVENTION: DIAGNOSTIC AND PROTECTIVE ANTIGEN GENE SEQUENCES OF TITLE OF INVENTION: ICHTHYOPHTHIRUS
TITLE OF INVENTION: ICANOPAPPER: 05/09/497,967
CURRENT APPLICATION NUMBER: 60/131,121
PRIOR FILING DATE: 1999-04-27
PRIOR FILING DATE: 1999-02-04
PRIOR FILING DATE: 1999-03-02
PRIOR FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 102
SCHWARE: PATENTIN VENTION: 2.1
SCHWARE: PATENTIN VENTION: 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 431, Application US/09886055
; Sequence 431, Application US/09886055
; GENERAL INFORMATION:
APPLICANT: STRYER, LUBERT
APPLICANT: STRYER, LUBERT
; TITLE OF INVENTION: BLOSENSORS OF CHEMICAL SENSORY PERCEPTION, AND
TITLE OF INVENTION: BLOSENSORS OF CHEMICAL SENSANTS
; TITLE OF INVENTION: BLOSENSORS OF CHEMICAL SENSANTS
; TITLE OF INVENTION: BLOSENSORS OF CHEMICAL SENSANTS
; CURRENT APPLICATION NUMBER: US/09/886,055
; CURRENT FILING DATE: 2001-06-22
; PRIOR PAPLICATION NUMBER: 60/213,812
; PRIOR PAPLICATION NUMBER: 60/213,812
; PRIOR PAPLICATION OF SEQ 1D NOS: 522
; NUMBER OF SEQ 1D NOS: 522
; SEQ 1D NO 431
; LENGTH: 975
                                                                                                                                 3832 GGAGACTGGGTCATCDCATAATAGATCAGGATCTTAGGCGCTTTCCA-----TGG 3881
                                            3782 DCTTGCAAGTGATAG-TGACCCTGTCTCCCA-----CCGATGCAGACAAGGATGAT 3831
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        382 CPAGTVLTDGTTSTYKQAASECVKCAANFYTTKQTDWVAGIDTCTSCNKKLTSGAEANLP 441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              307 QCNIACPDGTAIASGATNYVILQTECLNCAANFYFDGNNFQAGSSRCK-ACPANKVQGAV 365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                         ----ATAGGTATLIAQCALECPAGTVLTDGTTSTYKQAASECVKCAANFYTTKQTDWVAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match

8.3%; Score 212; DB 5;
Best Local Similarity 53.6%; Pred. No. 4.3e-11;
Matches 37; Conservative 12; Mismatches 20
                                                                                                                                                                                                                      3882 TTTCTGCTGDGTAGACAGTAATAAGTTGCGAA 3913
                                                                                                                                                                                422 IDTCTSCNKKLTSGAEANLPESAKKNIQCDFA 453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; ORGANISM: Ichthyophthirius multifiliis
US-09-497-967-12
                                                                                                                                                                                                                                                                                                                                   Sequence 12, Application US/09497967 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      442 ESAKKNIQC 450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 AEATQKVQC 69
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US-09-886-055-431
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US-09-497-967-12
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SERVING THE APPLICATION US/09500746

SENERAL INFORMATION:
APPLICANT: Winchester , Robert J.
APPLICANT: Winchester , Robert J.
APPLICANT: Gulko, Perrio
APPLICANT: Gulko, Perrio
TITLE OF INVENTION: USES OF INHIBITORS FOR THE ACTIVATION OF CXCR4 RECEPTOR BY SDF
TITLE OF INVENTION: TREATING RHEVMATOID ARTHRITIS
FILE REFERENCE: 0575/57005-B
CURRENT APPLICATION NUMBER: US/09/500,746
CURRENT APPLICATION NUMBER: US/09/500,746
SOFTWARE: PALENTING PATE: 2000-02-09
NUMBER OF SEQ ID NOS: 23
SOFTWARE: Patentin version 3.1
SEQ ID NO 1.00
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             352 CTCATGGC-----GTA-----CTA-----TGACCGCTATGTGGCT----GTGTG 383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    375 IAQCALECPA--GTVLTDGTTSTYKQAASECVKCAANFYTTKQTDWVAGIDTCTSCNKKL 432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     384 CAACCCICTACGGIACCCICTCCTCATGAACCGCAGGGITT-----GCITATICAIGG 436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -----TCTACCTGACCCTGATTGGAGGGGAATTCTTCCTGCTGGGT 351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               316 -TAIASGATNYVILQTECLNCAANFYFDGNNFQAGSSRCKACPANKVQGAVATAGGTATL 374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20 SANCPVGTETNTAGQVDDLGTPANCVNCQKNFYYNNAAAFVPGAS--TCTPCPQKKDAGA 77
                                                                                                                                                                                                               83 ATANLVIQCNVKCPAGTAIAGGAIDYAAIITECVNCRINFYNENAPNFNAGASTCTACPV 142
                                                                                                                                                                                                                                                              154 ATGGACTCC---CGCCTCCACACCCATGTACTTCTTGC---TCAGCCAGC-TCTCCAT 206
                                                                                                                                                                                                                                                                                                                  143 NRVGGALTAGNAATIVAQCNVACPTGTALDDGVTTDYVRSFTECVKCRLNFYYNGNNGNT 202
                                                                                                                                                                                                                                                                                                                                                                                                                       203 PFNPGKSQCTPCPAIKPANVAQATLGNDATITAQCNVACPDGTISAAGVNNWVAQNTECT 262
                                                                                                                                        23 CPVGTETNTAGQVDDLGTPANCVNCQKNFYYNNAAAFVPGASTCTPCPQKKDAGAQPNPP 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ---AGGACCTCCTGTCCAAGGACAAGACCATTTCCTTCCTGGGCTGTGCAGTTCAGATCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            263 NCAPNFYNNNAPNFNPGNSTCLPCPANKDYGAEAT ----AGGAATLAKQCNIACPDG--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9; Mismatches 180; Indels 116;
                                                         95;
Score 197.5; DB 5; Length 975; Pred. No. 1e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 410;
                                                                                                                                                                                                                                                                                                                                                                      207 CATGGATACCATCTACATCT---GTATCACTGTCCCCAAGATGCTCC----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
7.3%; Score 186; DB 5;
Best Local Similarity 25.1%; Pred. No. 3.5e-08;
Matches 102; Conservative 9; Mismatches 180.
                                                              6; Mismatches
                7.8%;
                   Query Match 7.8%
Best Local Similarity 23.9%
Matches 101; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 308 TCC-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; ORGANISM: Human
US-09-500-746-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            433 TSG 435
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US-09-500-746-17
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	91 GGMGICGNNGGAGCNGNIGIGAGIGGGAAGAAGGCNAC 128
н	138 TACPVNRVGGALTAGNAATIVAQCNVACPTGTALDDGVTTDXVRSFTECVKCRLNFYYNG 197
Н	129 GTCAANAAGGACGAATATTTGCAA
H	198 NNGNTPFNPGKSQCTPCPAIKPANVAQATLGNDATITAQCNVACPDGTI 246
H	155 NNGNNCAGGGCTGTNCNCGGGCAGTTTGTAAAAAAAAAAA
Ö	247 SAAGVNNWVAQNTECTNCAPNFYNNNAPNFNPGNSTCLPCPANKDYGAEATAGGAATL 304
6	213 AGTGINNGTIGACCCGAAGCNANAGIGGAINCAGGAGIAC-CIGGAGNNAACIAIGAACA 271
ñ	305 AKQCNIACPDGTAIASGATNYVILQTECLNCAANFYFDGNNFQAGSSRCKACPANKV 361
7	272 ANTAAGCGCAACAGCCAAAGAGGACTINCGGCTAGACCCACTGG 315
ñ	362 QGAVAȚAGGTATLIAQCALECPAGTVLTDGTTSTYKQAASECVKCAA 408
'n	316AGGAAAACTAAAACCTTGTGAGAGATGAAAGGNCAAAGA 354

Search completed: December 26, 2001, 10:38:18 Job time: 169 sec

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